

Abstract

Versions of the invention are directed to methods (including software), apparatus, compositions of matter, and new uses of compositions of matter for a new type of association based linkage study technique using bi-allelic markers. In this new type of association based linkage study technique, the bi-allelic markers used in the new linkage studies are chosen so that the least common allele frequencies of the markers vary systematically over a range or subrange of least common allele frequency and the chromosomal location of the markers vary systematically over one or more chromosomes or chromosomal regions. And the bi-allelic markers are chosen so that the markers' chromosomal locations and least common allele frequencies vary systematically in an essentially independent manner. This selection of markers achieves a systematic distribution of the markers over a two-dimensional region having the orthogonal dimensions of chromosomal location and least common allele frequency. By using the two characteristics or two dimensions of marker chromosomal location and marker allele population frequency in this unique way, the power and systematic nature of genetic linkage studies using association based linkage tests is greatly increased. These unique two-dimensional linkage study techniques increase the power of association based linkage studies to localize trait causing genes or polymorphisms of modest effect such as human disease causing polymorphisms.